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QY 363 DNPTMTFKEVTCPAELTTRSGCER 386
Db 196 DNPSINFNQVTCPSLTAKTNCKR 219

RESULT 2
Q9JH92 PRELIMINARY; PRT; 219 AA.
ID Q9JH92
AC Q9JH92
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL protists in the hindgut of termite Reticulitermes speratus.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045171; BAA98041.1; -
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
SQ SEQUENCE 219 AA; 23001 MW; 5F2EB81A6DE926CE CRC64;

Query Match 37.3%; Score 784.5; DB 14; Length 219;
Best Local Similarity 66.2%; Pred. No. 1.1e-42;
Matches 135; Conservative 29; Mismatches 37; Indels 3; Gaps 2;

QY 185 SGSTRYWDCKKASCSWPVKASVTGPVDTCASNGISLLDAN--AOSGCGNGGFMCMNNQ 242
Db 16 SGRTRYWDCKKASCAWEKKAATVPVDTCKAGDTRVASNDTVKSCDGGEGYCYDQA 75

QY 243 PVAVNDELAYGFAAASIAAGNEAGWCCGCGCYELTFTSGAASGKKMVQVNTTGGDLGSHNF 302
Db 76 PVAVNDVAYGFAAAACCG-GESGACCCYELTFTSGVNGKKMVQVNTTGGDLGSHNF 134

QY 303 DLOMPGGVGIFNGCAAGAPNDGWARYGGVSSVSDCASLPALQAGCKWRNFWPKNS 362
Db 135 DLAIPEGVGVIYNGCTQSGAPSDGWSRYGGVSSRSECSQLPSGLQAGCQWRFDWFQNA 194

QY 363 DNPTMTFKEVTCPAELTTRSGCER 386
Db 195 DNPSINFNQVTCPSLTAKTNCKR 219

RESULT 3
Q9JH91 PRELIMINARY; PRT; 219 AA.
ID Q9JH91
AC Q9JH91
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL protists in the hindgut of termite Reticulitermes speratus.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045172; BAA98042.1; -
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
SQ SEQUENCE 219 AA; 23003 MW; CA295CAD8F393199 CRC64;

Query Match 37.1%; Score 780.5; DB 14; Length 219;
Best Local Similarity 64.2%; Pred. No. 1.9e-42;
Matches 131; Conservative 33; Mismatches 37; Indels 3; Gaps 2;

QY 185 SGSTRYWDCKKASCSWPVKASVTGPVDTCASNGISLLDAN--AOSGCGNGGFMCMNNQ 242
Db 16 SGRTRYWDCKKSCGCKGWEKKAANDPKIDTCAKDGTRVASNDTVKSCDGGEGYCYDQT 75

QY 243 PVAVNDELAYGFAAASIAAGNEAGWCCGCGCYELTFTSGAASGKKMVQVNTTGGDLGSHNF 302
Db 76 PWQVSDSLSYGFAAAACCG-GESGACCCYELTFTSGVNGKKMIVQITNTGGDLGSHNF 134

QY 303 DLOMPGGVGIFNGCAAGAPNDGWARYGGVSSVSDCASLPALQAGCKWRNFWPKNS 362
Db 135 DLAIPEGVGVIYNGCTAQSGAPSDGWSRYGGVSSRSECSQLPSGLQAGCQWRFDWFQNA 194

QY 363 DNPTMTFKEVTCPAELTTRSGCER 386
Db 195 DNPSINFNQVTCPSLTAKTNCKR 219

RESULT 5
Q9JH87 PRELIMINARY; PRT; 219 AA.
ID Q9JH87
AC Q9JH87;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
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SQ SEQUENCE 219 AA; 23126 MW; A712EF3F3CAB041C CRC64;

Query Match 37.2%; Score 783.5; DB 14; Length 219;
Best Local Similarity 66.2%; Pred. No. 1.2e-42;
Matches 135; Conservative 31; Mismatches 35; Indels 3; Gaps 2;

QY 185 SGSTRYWDCKKASCSWPVKASVTGPVDTCASNGISLLDAN--AOSGCGNGGFMCMNNQ 242
Db 16 SGRTRYWDCKKASCAWEKKAATVPVDTCKAGDTRVASNDTVKSCDGGEGYCYDQA 75

QY 243 PVAVNDELAYGFAAASIAAGNEAGWCCGCGCYELTFTSGAASGKKMVQVNTTGGDLGSHNF 302
Db 76 PVAVNDVAYGFAAAACCG-GESGACCCYELTFTSGVNGKKMVQVNTTGGDLGSHNF 134

QY 303 DLOMPGGVGIFNGCAAGAPNDGWARYGGVSSVSDCASLPALQAGCKWRNFWPKNS 362
Db 135 DLAIPEGVGVIYNGCTQSGAPSDGWSRYGGVSSRSECSQLPSGLQAGCQWRFDWFQNA 194

QY 363 DNPTMTFKEVTCPAELTTRSGCER 386
Db 195 DNPSINFNQVTCPSLTAKTNCKR 219

RESULT 4
Q9JH89 PRELIMINARY; PRT; 219 AA.
ID Q9JH89
AC Q9JH89;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL protists in the hindgut of termite Reticulitermes speratus.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045174; BAA98044.1; -
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN_1.
SQ SEQUENCE 219 AA; 23033 MW; CA295CAD8F393199 CRC64;

Query Match 37.1%; Score 780.5; DB 14; Length 219;
Best Local Similarity 64.2%; Pred. No. 1.9e-42;
Matches 131; Conservative 33; Mismatches 37; Indels 3; Gaps 2;

QY 185 SGSTRYWDCKKASCSWPVKASVTGPVDTCASNGISLLDAN--AOSGCGNGGFMCMNNQ 242
Db 16 SGRTRYWDCKKSCGCKGWEKKAANDPKIDTCAKDGTRVASNDTVKSCDGGEGYCYDQT 75

QY 243 PVAVNDELAYGFAAASIAAGNEAGWCCGCGCYELTFTSGAASGKKMVQVNTTGGDLGSHNF 302
Db 76 PWQVSDSLSYGFAAAACCG-GESGACCCYELTFTSGVNGKKMIVQITNTGGDLGSHNF 134

QY 303 DLOMPGGVGIFNGCAAGAPNDGWARYGGVSSVSDCASLPALQAGCKWRNFWPKNS 362
Db 135 DLAIPEGVGVIYNGCTAQSGAPSDGWSRYGGVSSRSECSQLPSGLQAGCQWRFDWFQNA 194

QY 363 DNPTMTFKEVTCPAELTTRSGCER 386
Db 195 DNPSINFNQVTCPSLTAKTNCKR 219

RESULT 5
Q9JH87 PRELIMINARY; PRT; 219 AA.
ID Q9JH87
AC Q9JH87;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
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DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS Unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL protists in the hindgut of termite Reticulitermes speratus.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045176; BAA98046.1; -
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH 45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 219 AA; 23134 MW; 4BDEF4EC9ACC772D CRC64;

Query Match 37.0%; Score 779.5; DB 14; Length 219;
Best Local Similarity 63.0%; Pred. No. 2.2e-42;
Matches 133; Conservative 35; Mismatches 40; Indels 3; Gaps 2;

QY 178 ISGKSGSSTTRYWDCCKASCSPGKASVTGPVDTCSANGISLLDAN--AQSCGNGNG 235
DB 9 ISWSLADSGRTTRYWDCCKSGCGWEKKANVDKPIDTCAKDGTTTRVANSNDTVKSGCDGGD 68

QY 236 FMCNNPQWVNDLAYGFAAASITAGSNEAGWCGCYELFTSGAASGKKMVQVTTGG 295
DB 69 FMCYDQTFWQVSDSLSYGFAAAACCG-GESGACCGCYELFTSGPVNGKMWVQITNTGG 127

QY 296 DLGSHNFDLQMPGGGVIENGCAQWGPNDGARGYGVSSVSDCASLPALQAGCKWR 355
DB 128 DLGSHNFDLQMPGGGVIENGCAQWGPNDGARGYGVSSVSDCASLPALQAGCKWR 187

QY 356 FNFKNSDNPMTFKEVTCPAELTTRSGCER 386
DB 188 FDFQNDNPSINFQSCPSSEIIAKTNCNR 218

RESULT 6
QYJH90 PRELIMINARY; PRT; 219 AA.
AC QYJH90;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS Unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL protists in the hindgut of termite Reticulitermes speratus.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045173; BAA98043.1; -
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH 45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 219 AA; 23037 MW; 37E016415530A9A CRC64;

Query Match 36.7%; Score 772.5; DB 14; Length 219;
Best Local Similarity 63.7%; Pred. No. 6.2e-42;
Matches 130; Conservative 32; Mismatches 39; Indels 3; Gaps 2;

QY 185 SGSTRYWDCKKASCSPGKASVTGPVDTCSANGISLLDAN--AQSCGNGNGFMCNNQ 242
DB 16 SGKTRYWDCKKSGCGWEKKANVDKPIDTCAKDGTTTRVANSNDTVKSGCDGGTGMCYDOT 75

QY 243 PWAUNDELAYGFAAASITAGSNEAGWCGCYELFTSGAASGKKMVQVTTGGDLGSHNF 302

676 PMQVSDSLSYGFAAAACCG-GESGACCGCYELFTSGPVNGKMWVQITNTGGDLGSHNF 134
303 DLQMPGGGVIENGCAQWGPNDGARGYGVSSVSDCASLPALQAGCKWRNFWFKNS 362
135 DLAIPEGGVIENGCTAQSGAPSDGWSRGYGVSSRSECSQLPSGLQAGCQWRFDWFQNA 194
363 DNPTMTFKEVTCPAELTTRSGCER 386
195 DNPSINFNVKCPSEIIAKTNCNR 218

RESULT 7
QYJH95 PRELIMINARY; PRT; 217 AA.
AC QYJH95;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS Unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL protists in the hindgut of termite Reticulitermes speratus.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045168; BAA98038.1; -
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH 45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 217 AA; 22796 MW; 660DDI346B3769DE CRC64;

Query Match 36.5%; Score 769.5; DB 14; Length 217;
Best Local Similarity 64.7%; Pred. No. 9.5e-42;
Matches 132; Conservative 28; Mismatches 41; Indels 3; Gaps 2;

QY 185 SGSTRYWDCKKASCSPGKASVTGPVDTCSANGISLLDAN--AQSCGNGNGFMCNNQ 242
DB 14 SGKTRYWDCKKSGCGWEKKANVDKPIDTCAKDGTTTRVANSNDTVKSGCDGGTGMCYDOT 73

QY 243 PWAUNDELAYGFAAASITAGSNEAGWCGCYELFTSGAASGKKMVQVTTGGDLGSHNF 302
DB 74 PWGVDYSYALGFAGFAAASITAGSNEAGWCGCYELFTSGPVNGKMWVQVTTGGDLGSHNF 132

QY 303 DLQMPGGGVIENGCAQWGPNDGARGYGVSSVSDCASLPALQAGCKWRNFWFKNS 362
DB 133 DLAIPEGGVIENGCTAQSGAPSDGWSRGYGVSSRSECSQLPSGLQAGCQWRFDWFQNA 192

QY 363 DNPTMTFKEVTCPAELTTRSGCER 386
DB 193 DNPSMNFNVVSCPSSEIIAKTNCNR 216

RESULT 8
QYJH83 PRELIMINARY; PRT; 220 AA.
AC QYJH83;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS Unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RL protists in the hindgut of termite Reticulitermes speratus.";

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RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB045167; BAA98037.1; -
DR EMBL; AB045166; BAA98036.1; -
DR HSP; P43316; 2ENG.

DR InterPro; IPR000334; GH_45.

DR Pfam; PF02015; Glyco_hydro_45; 1.

DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.

SQ SEQUENCE 220 AA; 23108 MW; 97738D831BCFASF3 CRC64;

Query Match 36.4%; Score 766.5; DB 14; Length 220;

Best Local Similarity 64.2%; Pred. No. 1.5e-41;

Matches 131; Conservative 29; Mismatches 41; Indels 3; Gaps 2;

QY 185 SGSTRYWDCKKSCSWPKASVTGPVDTCSANGISLLDAN--AQSGCGNGGFMCMNNQ 242

DB 17 SGKTRRYWDCKKSCGWAKADVSKPIDTCAKDGTRVASNDTVKSGCDGGGYMCDYDQT 76

QY 243 PWAIVDELAYGFAAASAGNEAGWCCGCGYELTFTSGAAGKMMVQVNTGGDLGSHF 302

DB 77 PWGVNDSYALGFAAASAGNEAGWCCGCGYELTFTSGAAGKMMVQVNTGGDLGSHF 135

QY 303 DLQPGGGVIGFNGCAAGWAPNDGWARYGGVSSVSDCASLPALQAGCKWRNFWFKNS 362

DB 136 DLAIPEGGGVIGYNGCTAAGAPADGWGSGRYGGVSSRSCSLPSGLQAGCQWRFDWFQNA 195

QY 363 DNPMTTFKEVTCPAELTTRSGCER 386

DB 196 DNPINFNWVSCPSSELIKTNCRR 219

RESULT 9

Q9JH86

ID Q9JH86 PRELIMINARY; PRT; 219 AA.

AC Q9JH86;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Family 45 cellulase homologue.

OS unclassified eukaryotes.

OC Eukaryota.

OX NCBI_TaxID=42452;

RN [1]

RP SEQUENCE FROM N.A.

RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;

RT "Diverse genes of family 45 cellulase homologues of the symbiotic

protists in the hindgut of termite Reticulitermes speratus.";

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB045177; BAA98047.1; -

DR HSP; P43316; 2ENG.

DR InterPro; IPR000334; GH_45.

DR Pfam; PF02015; Glyco_hydro_45; 1.

DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.

SQ SEQUENCE 219 AA; 23158 MW; ECD686A8BED1DDI CRC64;

Query Match 36.3%; Score 764.5; DB 14; Length 219;

Best Local Similarity 62.7%; Pred. No. 2e-41;

Matches 128; Conservative 32; Mismatches 41; Indels 3; Gaps 2;

QY 185 SGSTRYWDCKKSCSWPKASVTGPVDTCSANGISLLDAN--AQSGCGNGGFMCMNNQ 242

DB 16 SGKTRRYWDCKKSCGWAKADVSKPIDTCAKDGTRVASNDTVKSGCDGGGYMCDYDQT 75

QY 243 PWAIVDELAYGFAAASAGNEAGWCCGCGYELTFTSGAAGKMMVQVNTGGDLGSHF 302

DB 76 PWSVNDYSYGFAPAAACCG-GEAGACCGCYDLTFTSGVPNGKHMIVQITNTGGDLGSHF 134

QY 303 DLQPGGGVIGFNGCAAGWAPNDGWARYGGVSSVSDCASLPALQAGCKWRNFWFKNS 362

DB 135 DLAIPEGGGVIGYNGCTAAGAPADGWGSGRYGGVSSRSCSLPSGLQAGCQWRFDWFQNA 194

QY 363 DNPMTTFKEVTCPAELTTRSGCER 386

DB 195 DNPINFNWVSCPSSELIKTNCRR 218

RESULT 10

Q9JH94

ID Q9JH94 PRELIMINARY; PRT; 221 AA.

AC Q9JH94;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Family 45 cellulase homologue.

OS unclassified eukaryotes.

OC Eukaryota.

OX NCBI_TaxID=42452;

RN [1]

RP SEQUENCE FROM N.A.

RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;

RT "Diverse genes of family 45 cellulase homologues of the symbiotic

protists in the hindgut of termite Reticulitermes speratus.";

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB045169; BAA98039.1; -

DR HSP; P43316; 2ENG.

DR InterPro; IPR000334; GH_45.

DR Pfam; PF02015; Glyco_hydro_45; 1.

DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.

SQ SEQUENCE 221 AA; 23220 MW; 8A84CEB0A8C46372 CRC64;

Query Match 36.2%; Score 762.5; DB 14; Length 221;

Best Local Similarity 63.2%; Pred. No. 2.7e-41;

Matches 129; Conservative 34; Mismatches 38; Indels 3; Gaps 2;

QY 185 SGSTRYWDCKKSCSWPKASVTGPVDTCSANGISLLDAN--AQSGCGNGGFMCMNNQ 242

DB 17 SGKTRRYWDCKKSCGWAKADVSKPIDTCAKDGTRVASNDTVKSGCDGGGYMCDYDQT 76

QY 243 PWAIVDELAYGFAAASAGNEAGWCCGCGYELTFTSGAAGKMMVQVNTGGDLGSHF 302

DB 77 PWAIVDSYSLGFAAASAGNEAGWCCGCGYELTFTSGAAGKMMVQVNTGGDLGSHF 135

QY 303 DLQPGGGVIGFNGCAAGWAPNDGWARYGGVSSVSDCASLPALQAGCKWRNFWFKNS 362

DB 136 DLAIPEGGGVIGYNGCTAAGAPADGWGSGRYGGVSSRSCSLPSGLQAGCQWRFDWFQNA 195

QY 363 DNPMTTFKEVTCPAELTTRSGCER 386

DB 196 DNPINFNWVSCPSSELIKTNCRR 219

RESULT 11

Q9JH88

ID Q9JH88 PRELIMINARY; PRT; 219 AA.

AC Q9JH88;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Family 45 cellulase homologue.

OS unclassified eukaryotes.

OC Eukaryota.

OX NCBI_TaxID=42452;

RN [1]

RP SEQUENCE FROM N.A.

RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;

RT "Diverse genes of family 45 cellulase homologues of the symbiotic

protists in the hindgut of termite Reticulitermes speratus.";

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB045175; BAA98045.1; -

DR HSP; P43316; 2ENG.

DR InterPro; IPR000334; GH_45.

DR Pfam; PF02015; Glyco_hydro_45; 1.

DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.

SQ SEQUENCE 219 AA; 23030 MW; 179BF1344C6D7024 CRC64;

Query Match 36.1%; Score 759.5; DB 14; Length 219;

Best Local Similarity 62.7%; Pred. No. 4.1e-41;

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Matches 128; Conservative 31; Mismatches 42; Indels 3; Gaps 2;
QY 185 SGSTRYWDCKKASCSPGKASVTGPDVTCAISNGISLLDAN--AQSNGNGGFMCMNNQ 242
DB 16 SGKTRTYWDCKKSCGHEKXANVDKPIDTCAKDGTTTRVANSNDTVKSGCDGGTYMCDQDT 75
QY 243 PVAVNDELAYGFAAASAGSNEAGWCCGCGCYELTFTTSGAASGKMWVQVNTTGGDLGSHNF 302
DB 76 PWQVSDSLSYGFAAACCAGG-GESGACCGCYELTFTTSGPVNGKMWIVQITTTGGDLGSHNF 134
QY 303 DLQMPGGGVIENGCAAGWAPNDGWRGARYGGVSSVSDCASLPSALQAGCKWRFNWFKNS 362
DB 135 DLATPGGGVGIYNGCTQSAGPADGWSRYGGVSSRSECCQLPSGLQAGCQWRFDWQNA 194
QY 363 DNPMTFKEVTCPAELTTRSGCR 386
DB 195 DNPMTFKEVTCPAELTTRSGCR 218

RESULT 12
ID Q9JH93 PRELIMINARY; PRT; 220 AA.
AC Q9JH93;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP "Diverse genes of family 45 cellulase homologues of the symbiotic
RT protists in the hindgut of termite Reticulitermes speratus."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045170; BAA98040.1; -
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH 45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 220 AA; 23091 MW; 35F174F9B79C2D65 CRC64;

Query Match 35.9%; Score 755.5; DB 14; Length 220;
Best Local Similarity 62.7%; Pred. No. 7.5e-41;
Matches 128; Conservative 31; Mismatches 42; Indels 3; Gaps 2;
QY 185 SGSTRYWDCKKASCSPGKASVTGPDVTCAISNGISLLDAN--AQSNGNGGFMCMNNQ 242
DB 17 TGRTRYWDCKKSCGHEKXANVDKPIDTCAKDGTTTRVANSNDTVKSGCDGGTYMCDQDT 76
QY 243 PVAVNDELAYGFAAASAGSNEAGWCCGCGCYELTFTTSGAASGKMWVQVNTTGGDLGSHNF 302
DB 77 PWGNDSPALGFAAASAGSNEAGWCCGCGCYELTFTTSGPVNGKMWIVQITTTGGDLGSHNF 135
QY 303 DLQMPGGGVIENGCAAGWAPNDGWRGARYGGVSSVSDCASLPSALQAGCKWRFNWFKNS 362
DB 136 DLATPGGGVGIYNGCTQSAGPADGWSRYGGVSSRSECCQLPSGLQAGCQWRFDWQNA 195
QY 363 DNPMTFKEVTCPAELTTRSGCR 386
DB 196 DNPMTFKEVTCPAELTTRSGCR 218

RESULT 13
ID Q9JH85 PRELIMINARY; PRT; 218 AA.
AC Q9JH85;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
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OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RT protists in the hindgut of termite Reticulitermes speratus."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045178; BAA98048.1; -
DR HSSP; P43316; 3ENG.
DR InterPro; IPR000334; GH 45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 218 AA; 22680 MW; A600FF5B990AD43 CRC64;

Query Match 35.6%; Score 750; DB 14; Length 218;
Best Local Similarity 63.1%; Pred. No. 1.7e-40;
Matches 128; Conservative 34; Mismatches 39; Indels 2; Gaps 2;
QY 186 GSTTRYWDCKKASCSPGKASVTGPDVTCAISNGISLLDANAQSGC-NGNGFMCMNNQPW 244
DB 17 GRTRYWDCKKSCGWDGKASVSKPVDTCADGTTRVATSAKSACDSGGTAYMCDQTPR 76
QY 245 AVNDELAYGFAAASAGSNEAGWCCGCGCYELTFTTSGAASGKMWVQVNTTGGDLGSHNF 304
DB 77 AVNDSYAIGFAAASAGSNEAGWCCGCGCYELTFTTSGPVNGKMWIVQITTTGGDLGSHNF 135
QY 305 QMPGGGVIENGCAAGWAPNDGWRGARYGGVSSVSDCASLPSALQAGCKWRFNWFKNSDN 364
DB 136 AIPGGVGLYNGCTQSAGPADGWSRYGGVSSRSECCQLPSGLQAGCQWRFDWQNA 195
QY 365 PTMTFKEVTCPAELTTRSGCR 387
DB 196 PSITFNEVSCPGDLTSTKTCRRQ 218

RESULT 14
ID Q9JH96 PRELIMINARY; PRT; 220 AA.
AC Q9JH96;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Family 45 cellulase homologue.
OS unclassified eukaryotes.
OC Eukaryota.
OX NCBI_TaxID=42452;
RN [1]
RP SEQUENCE FROM N.A.
RA Ohtoko K., Ohkuma M., Moriya S., Kudo T.;
RT "Diverse genes of family 45 cellulase homologues of the symbiotic
RT protists in the hindgut of termite Reticulitermes speratus."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045165; BAA98035.1; -
DR HSSP; P43316; 2ENG.
DR InterPro; IPR000334; GH 45.
DR Pfam; PF02015; Glyco_hydro_45; 1.
DR PROSITE; PS01140; GLYCOSYL_HYDROL_F45; UNKNOWN 1.
SQ SEQUENCE 220 AA; 23148 MW; 4F0652F8E8D269D5 CRC64;

Query Match 35.4%; Score 745.5; DB 14; Length 220;
Best Local Similarity 63.7%; Pred. No. 3.2e-40;
Matches 130; Conservative 27; Mismatches 44; Indels 3; Gaps 2;
QY 185 SGSTRYWDCKKASCSPGKASVTGPDVTCAISNGISLLDAN--AQSNGNGGFMCMNNQ 242
DB 17 SGRTRYWDCKKSCGHEKADVSKPIDTCAKDGTTTRVANSNDTVKSGCDGGTYMCDQDT 76
QY 243 PVAVNDELAYGFAAASAGSNEAGWCCGCGCYELTFTTSGAASGKMWVQVNTTGGDLGSHNF 302
DB 77 PRAVNDYALGFAAASAGSNEAGWCCGCGCYELTFTTSGPVNGKMWIVQITTTGGDLGSHNF 135
QY 303 DLQMPGGGVIENGCAAGWAPNDGWRGARYGGVSSVSDCASLPSALQAGCKWRFNWFKNS 362
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Db 136 DLAIPEGGVGYNGTAGAPADGWGSKYGGVSRSECSQLPSGLQAGCQWRFDWFOA 195
Qy 363 DNPTMTFKVETCPAELTTRSGCER 386
Db 196 DNPSINFNVVSCPGELIANTNCRR 219

RESULT 15

O93782 PRELIMINARY; PRT; 305 AA.
AC O93782;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Endoglucanase.
GN EGL3.
OS Humicola grisea var. thermoidea.
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
OX NCBI_TaxID=5528;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO9854;
RX MEDLINE=99144540; PubMed=990729;
RA Takashima S., Iikura H., Nakamura A., Hidaka M., Masaki H., Uozumi T.;
RT "Comparison of gene structures and enzymatic properties between two
RT endoglucanases from Humicola grisea";
RL J. Biotechnol. 67:85-97(1999).
DR EMBL; AB003107; BAA74956.1; -.
DR HSP; P43316; 2ENG.
DR InterPro; IPR000254; CBD fungal.
DR InterPro; IPR000334; GH_45.
DR Pfam; PF00734; CEM_1; 1.
DR Pfam; PF02015; Glyco hydro 45; 1.
DR ProDom; PD001821; CBD fungal; 1.
DR SMART; SM00236; fCBD_1.
DR PROSITE; PS00562; CBD FUNGAL; 1.
DR PROSITE; PS01140; GLYCOSYL HYDROL F45; 1.
SQ SEQUENCE 305 AA; 32174 MW; 28C979D6EDCD771D CRC64;

Query Match 34.1%; Score 718; DB 3; Length 305;
Best Local Similarity 61.7%; Pred. No. 2.5e-38;
Matches 127; Conservative 26; Mismatches 47; Indels 6; Gaps 3;
Qy 183 SGSGSTTRYWDCCKASCSWPGKASVTGPVDTCASNGISLLDANAQGCN-CGNGFMNNN 241
Db 21 AADGKSTRYWDCCPKSCGWAKAPVNPVFCNANFQRLTDFDAKSGCEPGGVAYSCADQ 80
Qy 242 QPWAYNDELAVGFAAASIAGSNEAGWCCGYELTFTSGAASGKKMVVQVNTTGGDLGSNH 301
Db 81 TFWAYNDDFAFGAATSAGSNEAGWCCACVYELTFTSGFVAGKKMVVQVSTSTGGDLGSNH 140
Qy 302 FDLQMPGGGVGFNCAQWGA-PNDGNGARYGVSVSDCASLPALQAGCKWRFNWFK 360
Db 141 FDLNIPGGGVGFIDGCTQFGGLP----GQRYGGISSRNECDRFPDALKPGCYWRFDWFK 196
Qy 361 NSDNPMTFKVETCPAELTTRSGCER 386
Db 197 NADNPSFSFRVQCPAELVARTGCR 222

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Job time : 33.4464 secs